GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - pr	OM protein – protein search, using sw model
Run on:	November 28, 2001, 19:50:29: Search time 10.4 seconds (without alignments) 494.070 Million cell updates/sec
Title:	US-09-516-052-2_COPY_28_177
Sequence:	1 REQDQYMPIANVIRIMRKTLYGYGMLDQSMVMGGGRYYQN 150
Scoring table:	BLOSUM62 Gapop 10.0 . Gapext 0.5
Searched:	93435 segs, 34255486 residues
Total number of	Total number of hits safisfying chosen parameters: 93435
Minimum DB seq length: 0 Maximum DB seq length: 2	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_39:*

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SEQUENCE
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi.
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Ol-NOY-1995 (Ref. 32) Last annotation update)
CCAMP-BINDING TRANSCRIPTION PACTOR CHRUNIT A (CHP A) (NE Y PROJETH
CUAIN B) (NE YB) (CAMI BOX DRA DIRETRO PROTEIN STRUNT B) (TEAGMENT)
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HSSP; P19267; IBFM.
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SUBUNIT: HETEROMERIC TRANSCRIPTION FACTOR COMPOSED OF TWO COMPONENTS, A ARD B, THAT ARD BOTH MIRED BY A GRA BURGING. SUBCELLULAR LOCATION: NUCLEAR, SUBCELLULAR LOCATION: NUCLEAR, SUBCRILITAR LOCATION: NUCLEAR, SUBCRITTOR BE SUBURILLY CONSERVED BOMAIN. THE BUSHALY CONSERVED A SOMAIN, THE BUSHALY CONSERVED BY SUBGRITTER BUSHALY CONSERVED A SOMAIN. THE BUSHALY CONSERVED A SOMAIN. THE BUSHALY CONSERVED AND SHA BUSHALK AND THE GUS KECH OF SCHAIR.
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>151
                                                 40.1%; Score 322.5; DB 1; 53.8%; Pred. No. 2.2e-22;
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01-JUL-1993 (Rel. 25) Last superior update)
01-GCT-2000 (Rel. 40) Last annotation update)
NTOTEAS TRANSPITTON FACTOR T SUBURIT AETA (HT Y FECTETH CHAIN F
(NF-YB) (CCAAT-BINGING TRANSPIPTION FACTOR SUBURIT A) (CBF-A) (C
                                                                                                                                                                                                                        the European Ricinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and the element entities requires a liberary arregard (See 181), [www.lst.s.lb.dl.and.or send an email to liberaredish sib ch).
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"Introl each organization of the NE Y genes.
modifies an activation domain.";
J. Biol. Chem. 257:8984-8990(1992).
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PIP: S22817: S22817.
HSSP: P19267: 1BFM.
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   Transcription regulation; DNA-binding; Activator; Nuclear protein.
                                                                  InterPro: IPR000947; -. Ptam: PF00808; CBFD_NFYB_HMF;
                                                                                                        MIM: 189904:
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                                  PROSITE: PS00685; CRFA_NEYB; ]
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SUBCELLULAR LOCATION: NUCLEAR.
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DOMAIN. THTEFACTION AND CHARINFIELD, AND THE THE FOR C FOMAIR
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Best Local Similarity
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DOMAIN
DNA_BIND
Vuorio T., Maity S.N., de Crombrugahe B.;

"purification and molecular cloning of the 'A' chain of a rat hoteromeric CCAAT-binding protein. Sequence identity with the yeast HAP3 transcription factor.";

I Biol. Chem 255:22480-22486(1990).

--- FUNCTION: STIMULATES THE TRANSCRIPTION OF VARIOUS GENES BY EECOGNIZING AND BINDING TO A CCAAT MOTIF IN PROMOTERS, FOR EXAMPLE IN TYPE I COLLAGEN, ALBUMIN AND BETA-ACTIN GENES.

--- SUBUNIT: HETEROMERIC TRANSCRIPTION FACTOR COMPOSED OF TWO
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01-ANG-1991 (Ref. 19, Last sequence update)
01-FEB-1996 (Ref. 33, Last annotation update)
CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CPE-A) (NF-Y PROTEIN
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MFDLINE=92195809; PubMed≃1549471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CHF-A) (NF-Y CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                   m afilities at.
                                                                                                                                                                                                                                                                                                                                                                                                                   Li X -Y , Maptowani B., Hoof' van Huijeduijnen P., Andre I.,
Benoist C., Mathis D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCB1_Tax1D=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; L
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse),
                                                                                                                                                   MEDLINE 91093096; PubMcd-2266139;
                                                                                                                                                                       SPECIES-Rat;
                                                                                                                                                                                    SEQUENCE FROM N A , AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                    Mathis D.;
                                                                                                                                                                                                                                                                                                      BRITGH
                                                                                                                                                                                                                                                                                                                   SPECIES-Mouse;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                      Wirlein Arids Fee 20-1087-1091(1992)
                                                                                                                                                                                                                                                                                                                                                                                       A-AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1/CBF) subunits."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Co-evolution from yeast to mouse open closing of the two NF-Y (CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     model van muljsdaljeer k., Li \mathbf{x}_{i}-V . Flick D . Matthes H., Benoist C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHLINE≃91006004; ÞybMed=1698608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NF.Y.B
                                                                                                                                                                                                                                                 "Intropyoyon organization of the Movy genee Tissue
                                                                                                                                                                                                                                                                                                                                                                                                yound tionary variation of the CCAAT binding transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 IIAELILWAMSKUUTENYVEELTVITASVEKTETETEKSSALKSUSSESLEGTYSSÄMSTS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 REGIDTYLETIANVARTMENATEGISKTAKFARECVOECTVSEETSETTSEASERGEGEGERRET 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 PECCECAMPIANCIE IMPETITESHAFISCIAFETT JEGVETET SEVEGEAMPROGET (PROFILE) 60
                                                                                                                                                                                                                    Biol Chem 267:8984-8990(1992).
                                                                                                                                                                                                                                                                                  X. Y., Hooft van Huijsduijnen R., Mantovani R., Benoist C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INGEDILFAMSTLGEDSYVEPLKLYLQKERE-----AMKGE-------KGIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3119 3127(1990)
                                                                                                                                                                                                                                                                                                      92250498; FubMod 1577736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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59
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22831 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Battus norvegious (Pat).
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INTELANT
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1 JAN 1995 (Ref. 18, Last sampled or update)

1 JAN 28906 (Ref. 40, Last sampled or update)

1 PANSTEDETIONAL ACTIVAL de HAFE (HASZ REDHLADGEY FECTEIN A)

RAPES OF YRLUGET OF YRLUGET.
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P13434;
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                             Hills 3.5 Finkham 1.5 West E.5 Miller R.5 Sharrester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaromyces cerevisiae (biker's yeast).
Bukaryota: Bungi: Ascomptota: Saecharomycetina: Saecharomycetes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRANGA ( ) GOSTO.
MODE MOTESTATE NESSE
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COMPONENT OF THE HIGHTS OF VARIABLE AND SELECTIONS.

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COMPONENTS OF THE HIGHTS OF VARIABLE AND SELECTIONS.

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COMPONENTS OF THE HIGHTS OF VARIABLE AND SELECTION OF THE S
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PTR; A28123; A28123.
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EMBL: Z35782;
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96 INGELILISTHALGEBNYAEVIKTYLAKYEG 126
                                                                              61 TTABBILLWAMSKLGFBNYVDPLTVFINKYRE 91
                                                                                                                                                        56 EBBELOW, 61 SVICTA OSTITIKA OPWINING WASHING HARMINIVARING CONTROL OF THE CONT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PECCRORY CIRT MITTELL I
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                                                                                                                                                                                                                                                                                                                                                                     $4.6%; Secto 280; DR 1; 56.0%; Prof. No. 1.4e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIOME, D., Churcher C.M., Barrell B.S., Rajandream M.A., Wood V.: Schmitteld (AUTHING) to be EMMI, "Subject," Inv. Jarahasov, Charletton: BELONGS TO A COMPLEX THAT BINDS TO THE SUBJECTED LOCATED UPSIREAM OF GENES INVOLVED IN MITOCHONDRIAL ELECTRON
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Eukaryota: Finyl: Ascomyceta: Schizosaccharomycetales: Schizosaccharomycetaleae;
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01-JUN-1994 (Rel. 29, last sequence update)
01-OCT-2000 (Rel. 40, last anoutation update)
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HSSP; P19267; 1BFM.
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                                                                                                                                                                                                                                                                                                                                    FRANSFAC: F01263;
 12 LPTAMVARIMKSALPENAKTSKEAKTOVOUGUSTSELISEVIGLASEQGIQERRRIIIGELA 71
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Pred. No. 1.2e-18;
Pred. No. 1.2e-18; Indols
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Eukaryetomyces lactis (Yeast).

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P40914,
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MEDICINE 97,4797; PERMOND 7845762;
Mulder W., Scholten I.H.JM., de Boer R.W., Grivell L.A.;
"Sequence of the HAP3 transcription factor of Kluyveremyves lactis
"requence the presence of a newel 4 cysteine zinc-finder motif.";
Mod Common Area 66 1967 1964
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01 FEB-1995 (Rel. 31, Tast sequence update)
15-DEC-1998 (Rel. 37, Tast annotation updat
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PROSITE; PS00685; CBFA_NFYB; 1.
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PIR: $41926; $41926.
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-!- FUNCTION: BINDS TO THE UPSTREAM ACTIVATION SITE (UAS) OF THE CYCL
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92 NOEDTILSTUALCIENYAEVIKTYLAKYPQ 111
                                                      62 TALLILWAMSKIGITUNYVDFITVFINKYRE 91
                                                                                                       DOMAIN: CAN BE DIVIDED INTO THREE DOMAINS. THE WEAKLY CONSERVED DOMAIN, THE HIGHLY CONSERVED B DOMAIN THOUGHT TO BE INVOLVED IN SUBUNIT INTERACTION AND DNA BINDING, AND THE GLU-RICH C DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENE AND OTHER GENES INVOLVED IN MITOCHONDRIAL ELECTRON TRANSFORT AND ACTIVALIST THERE EXISTS STANDARD CRAFF THE SECURICAL COMPLEX (FY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     α
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                         124
156
205 AA;
                                                                                                                                                                                                                     Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
111
27
54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205
65
                                                                                                                                                                                                                                                                                                                                                               13122 MW/
                                                                                                                                                                                                                                               33.5%; Score 269; DB 1; 54.4%; Pred. No. 2.1e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                   ASP/GLU-RICH (ACIDIC).
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
IMPORTANT FOR SUBUNIT INTERACTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (HY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                            B33C7BEFBEID7EIA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205
                                                                                                                                                                                                                                                                         DB 1; Length 205;
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OF MAY 1992 (Bol. 22) (Toutod)
OF MAY 1992 (Bol. 22) Last sequence update)
OF MAY 1992 (Bol. 22) Last sequence update)
OF MAY 1992 (Bol. 22) Last sequence update)
o) JHL 1993 (Rel. 25, Steated)
o) HU, 1993 (Rel. 25, Last Sequence update)
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                                                                 NVWOR HOWER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by entitles requires a liceuse agreement (See http://www.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation the European Ricinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xemopus laevis (African clawed frog).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                             REGIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nº X I III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS PROTentry is copyright. It is produced through
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li X. Y., Mantovani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDICANE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ampdribia; Batrachia; Amara; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERSENT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VINEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; DNA binding; Activator; Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Evolutionary variation of the CCAAT binding transcription factor
                                                                                                                                                                                                                                                                                                                                                        local Similarity
                                                                                                                                                                                                             94 TURGSALRGEPPSLEQTYGGNGIG 117
                                                                                                                                                                                                                                                                                           44 TOPOVSEYTSFVEDEANEROOREORETITAEDILMAMSELGENNYVDPLTVFINRYRETE 93
                                                                                                                                                                                                                                                    | VQBTVSKF1SF1TSEASEROTIQEKKK11NQEDILFAMS11AFDSYVEYLKIX1QKFRE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN. CAN HE DIVIGED INTO THREE DOMAINS: THE WEAKLY CONSERVED DOMAIN, THE HIGHEY CONSERVED B DOMAIN THOUGHT TO BE INVOLVED IN SUBJUNIT IN JUNEAU IN A DINIONES, AND THE GLE RICH C DOMAIN. SIMILARITY: RELOADES TO THE CHE A SUBJUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECOGNIZING AND BINDING TO A CCAAT MOTIF IN PROMOTERS, FOR EXAMPLE IN TYPE I COLLAGEN, ALBMINI AND RETA-ACTIN GENES. SHHUNIT: HEITER-MERIC TRANSCRIPTION FACTOR COMPOSED OF TWO COMPONENTS, A AND B. THAT ARE BOTH NEEDED FOR DNA BINDING SHREELULIAR LOWALION. NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: STIMULATES THE TRANSCRIPTION OF VARIOUS GENES BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8228193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X59709; CAA42229.1;
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                                                                                                                                                                         AMKGEKG1GG1VI1GDGLG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                          122 AA: 13498 MW; E76AB9FB6638F53A CRC64;
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                                                                   STANIARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20:1087 1091(1992)
                                                                                                                                                                                                                                                                                                                                                        27.9%; Score 224.5; bis l; longth 122; 51.2%; Pred, No. 1.16-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Weelt van Holljsdeljmen R., Andre I
                                                                                                                                                                                                                                                                                                                                       Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C DOMAIN.
                                                                                                                                                                                                                                                                                                                                                      Pred, No.
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DR1_ARATH
ID DR1_A
AC P4959
DT 01-FE
DT 01-FE
DT DR1_P
GN DR1_P
GN DR1_OS
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OC Bikar
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Best Local Similarity
                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                             P49592;
                                                                                                                                                            DR1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIWMOOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transcription; Phosphorylation; Nuclear protein.

SIMILAR | 100 | SOME, TO YEAST HADS PROTEIN (AA 30-181).

DOMAIN | 100 | 101 | NUCLEAR FORMAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PROUGHTS; CEATSUBUNTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 601482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a livense agreement (See Lttp. or send an email to licensewisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of class II gene transcription.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFAC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-007-2000 (Rel. 40, Last annotation update)
TATA-BINDING PROTEIN-ASSOCIATED PROSPHOPROTEIN (DOWN-REGULATOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR000947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inostroza J.A., Mermelstein F.H., Ha L., Lane W.S., Reinberg D.;
"Drl, a TATA-binding protein-associated phosphoprotein and inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MED4.INE 92354065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEÇUENJE ENDENIA.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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                                                                                                                                                                                                                                                                  67 SPEHVIOALESLGEGSYISEVKEVLOECKTVALKERKA 104
                                                                                                                                                                                                                                                                                                          62 TAEDILWAMSKIGFDNYVDPLTVFINFYREIETDRGSA 99
                                                                                                                                                                                                                                                                                                                                                   8 DDDL1 IPRAATNKMIKETLP-NVRVANDARELVVNCCTEFIHLISSEANEICNKSEEKTI 66
                                                                                                                                                                                                                                                                                                                                                                                        2 EQIQYMPIANVIRIMEKTI DSHAKIS DAKETI OECVSEYISEVIGEANEECQEEGEETI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUNCTION: THE ASSOCIATION OF DRI WITH THE RESULTS IN A FUNCTIONAL REPRESSION OF BOTH ACTIVATED AND BASAL TRANSCRIPTION OF CLASS IL GENES. THE INTERACTION OF DRI WITH THE PRECLIDES THE FORMATION OF A TRANSCRIPTION COMPETENT COMPLEX BY INHIHITING THE ASSOCIATION OF THE LAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHRUNIT: DRI EXISTS IN SOLUTION AS A HOMOTETRAMER THAT LISSOCIATES DURING INTERACTION WITH TBP AND THEN, AFTER COMPLEXING WITH TBP, BRASSOCIATES AT A SLOW RATE, TO RECONSTITUTE THE TETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: PHOSPHORYLATION REGULATES ITS INTERACTION WITH TBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T00197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 103 N
121 168 A
176 AA; 19443 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO A.THALIANA DRI HOMOLOG AND TO YEAST HAD I PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMod 1339312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.1%; Secre 161.5; DB 1; Length 176; 28.5%; Pred. No. 7.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36E7E59F2PD6CAB5 CRC64;
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                                                                                                                                                                 159 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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Arabidopsis thaliana (Mouse ear cross). Enkaryota; Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;

DRI PROTEIN HOMOLOG.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a line sensition of (85% LUTE 2000) isb
                                                          STRAIN-VO-16 / GSM 4304 / AICT 43058,

MEDLINE-98049443. FubMad-9389475.

Klenk H - P. Clayton R A. Tamb J - F. White O., Nelson K.E.,

Klenk H - P. Clayton R A. Tamb J - F. White O., Nelson K.E.,

Ketchum K.A. Ledson R I. Galun M , Hackey E K , Peterson J.D.,

Ketchum K.A. Ledson R I. Galun M , Hackey E K , Peterson J.C.,

Floischmann R.D., Gudson R I. Galun H , Sutton G.C., Cill S.,

Floischmann R.D., Gudson K , McKenney K , Adams M.D., Loftus B ,

Peterson S. Beich G.I. McWeil in K , Bodder I H , Glodok A , Zhon

Operbeck F , Golupte J F , Wilholm F , McDenald L , Heterlea F T ,

Sadow P.W., D'Andrea K.P., Bowman C , Fujii C , Garland S.A.,

Sadow P.W., D'Andrea K.P., Bowman C , Fujii C , Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piam; PE00808; CBFD_NEYB_HME; 1.
Transcription: Nuclear protein.
SEQUENCE 159 AA; 17942 MW; B5BCEC9E9BBE54FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to licensewisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCHI_TaxID:3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Magnoliophyta, endicotyledons, core endicots; Rosidae; curosids H: Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
310-MCT-2000 (Rel. 40, Last annotation update)
PROBABLE ARCHAEAL HISTONE Al-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAF2_ARCEU
028779;
                                                                                                                                                                                                                                                                                                                                                                                                         Archaea: Euryarchaesta: Archaesqlobales, Archaeoglobasca
                                                                                                                                                                                                                                                                                                                                                                                                                               Archaeoglobus fulgidus.
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reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                       Archaeoglobus
                        "The complete genome sequence of the hyperthermophilic, sulphate
                                                 Venter J.C
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SUBCELLULAR LOCATION: MUCLEAS (5Y
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25.6%;
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Pred. No. 1.3e-07;
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Matches 24, Conset.
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-i- FUNCTION: BINDS AND COMPACT DNA (95 TO 150 BASE PAIRS) TO FORM NUCLEOSOME-LIKE STRUCTURES THAT CONTAIN POSITIVE DNA SUPERCOLLS INCREASES THE RESISTANCE OF DNA TO THEMMAL DENATURATION (HY
                                                                                                                                                                              Richk H.-P. Clayton P.A., Tomb J.-P., White O., Nelson K.E., Ketchum K.A., Dodson P.T., Gwinn M. Hickey F.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Picschmann R.D., Duackenbush J. Lee N.H., Sutton G.G., Gill S., Pirknoss E.F., Daugherry R.A., McKenney K., Adams M.D., Loftus B., Peterson S., Peich C.I., McNeil L.K., Hadger J.H., Glodek A., Zhou L., Cwerbeek P., Gorayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andron K.P., Rowman C., Priji C., Carland S.A., Wasson T.M., Olsen G.J., Fraser C.M., Smith H.O., Wocse C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation that Phryphana Bioinformatics institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
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Pfam; PF00808; CRFD_NEVB_HME; ].
CNA 53531ng - Multimono family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P48781; 1HTA.
TIGR; AF1493; -.
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                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049344: PubMed=0389475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
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                                                                                                                                                                     Venter J.C.
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                                                                                                       Nature 300-364-370(1997)
                                                                                                                         "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.":
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                                                           FUNCTION: BINDS AND COMPACT DMA (95 TO 150 BASE PAIRS) TO FORM NUCLEOSOME-LIKE STRUCTURES THAT CONTAIN POSITIVE DMA SUPERCOILS
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SIMILARITY: RELONGS TO THE HMF FAMILY OF ARCHAEAL HISTONES
                   SIMILARITY)
                                         INCREASES THE RESISTANCE OF DNA TO THERMAL DENATURATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MPIAHVIETHERTELECHAKISDOARPTOPSTYBSVORSTARAKORISDAKTELTARDI 66
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39, Last sequence update)
40, Last annotation update)
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"Burification and characterization of a histone like protein from the
Archaeol isolate ANL, a member of the Thermococcales.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or MAY 2000 (Ref. 6). Teated)
Of MAY 2000 (Ref. 6). Last sequence update)
Of off 2000 (Ref. 45, last annotation update)
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SEQUEENE 72 AA: 2005 NW. 1A075BABSE22E030 (No.4.
                                                                                                                                                                                                                                                                                 MEDIJNE 97014371: Fishmod 8861206;
                                                                                                                                                                                                                                                                                                                                                                Biochim, Biophys. Acta 1867:1-7(1996).
                                                                                                                                                                                                                                                                                                                                                                                 "A dency handA, encoding an archaeal histone like protein from the
Thermoreness species ANT: homology with cukaryal histone consenses
acqueeness and the implications for delineation of the histone fold.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEJUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / METANVIRIMERITIESHAKTSHAKETIQESTYSEVISEVISIANER QKEQRKITTAEDI 66
                                                                                                                                                            NUPLESCEME LIKE STORTHERS THAT CONTAIN FOSTITVE DNA SHERKOTIS. MICHESCEME LIKE STORTHERS THAT CONTAIN FOSTITVE DNA SHERKOTIS.
                                                                               SIMILARTEY, BEHARES OF THE HME PAMILY OF AFTHARAL BISTONES
                                                                                                    COURGINALLY RELEASE ACTIVITY.
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                                                                                                                                        INCREASES THE RESISTANCE OF DNA TO THERMAL DENATURATION (BY
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$1,8%; Pred. No. 0.082;
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                                                                            Overy Match 11.1%, Score 89: DB-1:
Hest Local Similarity 35.9%; Pred. No. 0.082:
Matches 24: Conservative 15: Mismatches
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Best Local :
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                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                    modified and this statement is for removed. Usage by and for communications requires a license agreement (20-10) [[]*** []*** []*** []*** or send an email to license tisbesib.eth).
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01-007-1996 (Rel. 4) Last seq
01-007-2000 (Rel. 40, Last anno
                                                                                                                                                                                                  DNA-binding: Multigene tamily
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Pram; PF00808; CHFU_NFYH_HMF; 1.
                                                                                                                                                                                                                                                             EMBL: 008837; AAA73426.1; =.
HSSP: P19267; IBFM.
                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HMI tamily of archaeal histones in a non-methanogenic Archaeon
Gene 150:207-208(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus \operatorname{Sp.} (strain ob sa). Archaea: Buryarchaeota: Thermococcus Thermococcus occus.
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PS0485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sandman K.M., Perler F.B., Reeve J.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE 95047544; PubMed 7959058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE TRAM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID 55399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 66 AA; 7205 MW; C84C4DF62305D5AO CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Histone encoding genes from Eyrococcus: evidence for members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            We bounding, Multigene family.
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4 LPTAPVDRLIEKA -CAERVSEEAARTLAHYLEEYATEVSEKAVEFARHACKKIVKARDI 61
                                      7 METANVIRIMETLESHAKISDIAKETIGE VSEYTSEVICEANERGGEGRETICAEDI 66
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